

BLASTP ALIGNMENT OF SEQ ID NO: 6 INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN-LIKE POLYPEPTIDE (IDENTIFIED AS IGFBP-7-HY1) WITH MUS MUSCULUS INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN SEQ IN NO:13

Query: IGFBP-like protein [SEQ ID NO: 6)
Subject: >gi|9055246 (AB006141) IGFBP-like protein [Mus musculus] SEQ ID NO: 13
Length = 270

Score = 1170 (416.9 bits), Expect = 1.8e-118, P = 1.8e-118
Identities = 209/269 (77%), Positives = 232/269 (86%)

Query: 8 LP^LL^LL^LL^LP^LL^LP^LL^LP^LL^LG^IR^DV^GG^RR^PK^CC^PR^PE^GC^PA^PC^PA^PG^IS^AL^DE^CG^CC^A 67
+P L LLLL LLP L+ LG+RD G R P+C PC+ + CPAP+PCPAP ISA DECGCCA
Sbjct : 1 MPR^LP^LL^L-L^LP^LL^L-L^LP^LL^L-L^LP^LL^LG^IR^DA^GR^RH^PE^CS^PC^QQ^DR^CP^AP^SP^CP^AF^DE^CG^CC^A 59

Query: 68 RCLGAEGASCGGRAGGRCGPGLVCASQAAGAAPEGTGLCVCAQRGTVCGSDGRSYPSVCA 127
RCLGAEGASCGG G RCGPGLVCAS+A+G APEGTGLCVCAQRG VCGSDGRSY S+CA
Sbjct : 60 RCLGAEGASCGGPVGSRCGPGLVCASRASGTAAPEGTGLCVCAQRGAVCGSDGRSYSSICA 119

Query: 128 LRLRARH^TPRAHPGHLHKARDGPCEFAPVVVVPPRSVHNVTGAQVQVGLSCEVRAVPTPVIT 187
LRLRARH PRAH GH^IHKARDGPCEFAPVV++PPR + HNVTG QV LSCEV+AVPTPVIT
Sbjct : 120 LRLRARH^APRAHGH^IHKARDGPCEFAPVVLMPPRDIHNVVTGTQVFLSCEVKAVVPTPVIT 179

Query: 188 WRKVTKSPEGTQALEELPGDHVNIAVQVRGGPSDHEATAWILINPLRKEDEGVYQCHAAN 247
W+KV SPEGT+ LEELPGDHVNIAVQVRGGPSDHE T+WILINPLRKEDEGVY CHAAN
Sbjct : 180 WKKVKHSPEGTEGLEELPGDHVNIAVQVRGGPSDHETTSWILINPLRKEDEGVYHCHAAN 239

Query: 248 MVGEAESHS^TTVLDSLKYRSFHF^PA^PDD 276
+GEA+SH TVTVLDL+Y+S + P D

Sbjct : 240 AIGEAQSHGT^TTVLDLNRYKSLYSSVPGD 268

FIG. 1

BLASTP ALIGNMENT OF SEQ ID NO: 6 INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN-LIKE POLYPEPTIDE (IDENTIFIED AS IGFBP-7-HY1) WITH HOMO SAPIENS PROSTOGLANDIN I2 SEQ NO: 14

Query: IGFBP_like protein (SEQ ID NO: 6)
Subject: >gi|1082724 Prostaglandin I2 [Homo sapiens (SEQ ID NO: 14)]
Length: 273

Score = 570 (205.7 bits), Expect = 7.9e-61, P = 7.9e-61
Identities = 123/273 (45%), Positives = 150/273 (54%)

Query: 4 PSLRALLGAAAGLLILL--PLSSSSS-SDT-----CGPCEPASCPPIPPPLGCLLGETR 54
P L +LLL LLL L PLS S D CGPC P CP P
Sbjct : 2 PRL-SLLLPLLPLLPLL.PLSPSLIGIRDWGRRPKCGPCRPEGCPAPACPAPGISA L 60

Query: 55 DACGCCPMCARGEPEPGGGAGGRGYCAPGMECVKSRSRKRRKGKAGAAAGGPGVSGVVCCK 114
D CGCC C EG CGG GR C PG+ C AGAA G +G+CVC
Sbjct : 61 DECGCCARCLGAEGASCGGRAGGR--CGPGLVCA SQA----AGAAPEG--TGLCVCA 109

Query: 115 SRYFVCGSDGTTYPSSGCQLRAASQRAESRGKEKAITQVSKGTCEQGPSTIVTPPKDIWNNTG 174
R VCGSDG +YPS C LR ++ + + G CE P +V PP+ + NVTG
Sbjct : 110 QRGTIVCGSDGRSYPSVCA LLRARHTPRAHPGHHLHKARDGPCEFA PVVVVPPRSVHNTTG 169

Query: 175 AQVYLSCEVIGIPTPVLIWNKVKRGHYGVQRTTELLPGDRDNLAIQTRGGPEKHEVTGWVL 234
AQV LSCEV +PTPV+ W KV + G Q E LPGD N+A+Q RGGP HE T W+L
Sbjct : 170 AQVGLSCEVRAVPTPVITWRKVTKSPEGTQALEELPGDHNIAVQVRGGPSDHETAWIL 229

Query: 235 VSPLSKEDAGEYECHASN SQQQASASAKITVVD 267
++PL KED G Y+CHA+N G+A + + TV+D
Sbjct : 230 INPLRKEDEGVYQCHAANMVGAEESHSTVTL D 262

FIG. 2